MINAR International Journal of Applied Sciences and Technology
ISSN: 2717-8234
Article type: Review article

Received: 06/07/2022 **Accepted:** 29/07/2022 **Published:** 01/09/2022

FRONTIERS IN EARLY DETECTION OF HEPATOCELLULAR CARCINOMA

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Abstract

It is the most common cancer in the world, and in the United States it is the fifth most common. It is common for liver cancer patients to be diagnosed at an advanced stage, which has a negative impact on their prognosis. Hepatocellular carcinomas (HCCs) account for more than 90% of all liver cancer cases, and chemotherapy and immunotherapy are the most effective treatments. Patients with liver cancer need new therapeutic choices. It's possible that natural chemicals and/or nanotechnology can improve patient outcomes while minimizing negative effects. Improved treatment options can lead to better outcomes. This study concludes by highlighting a few of the challenges people with liver cancer face, as well as some promising new treatments.

Keywords: Hepatocellular Carcinoma, Alpha Fetoprotein, Molecular Tools, Protein And Non-Protein Tools, Apoptosis, Lysosomal Enzymes, Extracellular Matrix.

http://dx.doi.org/10.47832/2717-8234.12.22

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Introduction

Excessive extracellular matrix protein buildup is a hallmark of hepatic fibrogenesis, a pathophysiological result of chronic liver damage. Hepatic cells (hepatocytes), stellate cells, sinusoidal endothelial cells, and immune cells (resident and invading) all play a role in the dynamic process of fibrosis. To better understand liver fibrosis, this review focuses on the role of cell types, cytokines and chemokines, and what it takes for fibrosis to regress. Hepatic stellate cells have distinct mitochondria and metabolic alterations that influence the fibrogenic process, which we examine here. The role of fibrosis in the development of hepatocellular carcinoma is also briefly discussed [1].

Cirrhosis, portal hypertension, and liver failure are all common outcomes of advanced liver fibrosis, which frequently necessitates a liver transplant. Another key risk factor for hepatocellular carcinoma is advanced hepatic fibrosis and necrosis (HCC). Pathogenesis of liver fibrosis hinges on the function of hepatic stellate cells (HSCs). oxidant stress, mitochondrial dysfunction, and metabolic remodeling all influence the activation of HSCs in the liver, and our study summarizes these pathways and identifies possibilities for therapeutic intervention [1].

As hepatocellular carcinoma (HCC), a tumor of the parenchymal cells of the liver, it is believed to be malignant. It is the fifth most common cancer in humans worldwide [2] and the second greatest cause of cancer-related death [3]. HCC tumors can spread into the liver by migrating to the liver from other tumors, creating new tumor colonies that can be difficult to identify because of the widespread usage of AFP in all phases of the disease. AFP is only created from primary, not secondary, hepatocarcinoma [4]. This is owing to a surprising truth. However, in both clinical and experimental settings, AFP is widely employed as a first diagnostic characteristic to link hepatocyte carcinogenesis [5]. Small RNAses, single nucleotide polymorphisms (SNPs), survival/apoptotic rates, DNA replication error-correcting enzymes, the integrity of lysosomal membrane and its released enzymes, extracellular proteins and the family of enzymatic processes that affect its integrity are among the variables that we will discuss here.

There are more than 700,000 cancer-related fatalities per year due to hepatocellular carcinoma (HCC), the most common form of primary liver cancer [6,7,8]. The prevalence of HCC has increased significantly in the United States and Europe over the past two decades [6,7]. Tumor excision, liver transplant, chemotherapy, and radiology are the primary treatment choices for patients with early-stage illness at this time. However, the vast majority of HCC patients are detected at advanced stages, which do not have curative treatment options [8,9,10,11]. As a result, lowering the high death rate necessitates early detection and prevention of HCC. Preventive therapeutics targeting particular HCC-promoting variables must be developed in order to improve prognosis. A deeper knowledge of the molecular basis of HCC formation and the identification of markers are necessary.

HCC has been linked to cirrhosis, an inflammation of the liver in which normal liver tissue is replaced by scar tissue and regenerative nodules, as a result of long-term damage caused by various etiologies, including hepatitis B (HBV) or C (HCV) viral infection, chronic alcohol consumption or nonalcoholic fatty liver disease [11,12,13]. There is evidence that cirrhosis plays an important role in hepatocarcinogenesis, as up to 90% of all instances of HCC occur in people with this liver condition [6,7,8]. Cirrhosis is accompanied with numerous cycles of cell death, inflammation, and compensatory hepatocyte growth at the cellular level, which results in the formation of regenerative nodules and fibrous bands in cirrhotic livers. To summarize, the regenerative nodules contain a variety of cell types that are capable of proliferation (such as stem cells), newly generated hepatocytes, and cells that are resistant to apoptosis (such as those that have been injured by apoptosis) [12,14]. The precancerous state of cirrhosis is therefore recognized and is relevant for the research of genetic markers of HCC

development and prevention measures. Although the underlying molecular pathways of liver cirrhosis development to HCC have been published in detail, the etiology and clinical features of this condition remain largely unclear.

After a long period of steady accumulation of genetic and epigenetic abnormalities in the liver cells, HCC develops slowly and unrestrained proliferation of mature liver cells occurs. In HCC cells, an increase in glycolysis and lactate generation is one of the most prevalent metabolic alterations identified [15,16,17,18]. It is nevertheless possible to experience the Warburg effect or aerobic glycolysis in the presence of sufficient oxygen and mitochondria that operate properly [19,20,21,22]. The tricarboxylic acid (TCA) cycle and oxidative phosphorylation (OXPHOS) produce carbon dioxide in the mitochondria during aerobic glucose metabolism, whereas the liver's normal differentiated hepatocytes convert glycolysis-derived pyruvate into lactate under low oxygen conditions. Regardless of oxygen supply, HCC cells appear to re-adjust their energy metabolism by switching to glycolysis [17,18]. The pentose phosphate pathway (PPP) produces the cellular reductant NADPH and macromolecules (nucleotides, amino acids, and fatty acids) necessary for doubling biomass and inhibiting apoptosis in HCC cells when the metabolic shift occurs in these cells [18,23,24].

It has been established that oncogene activation or loss of tumor suppressors alters cell metabolism by changing the expression and activity of enzymes that stimulate glucose intake. The principal glucose transporter GLUT1 is up-regulated in HCC cells, resulting in an increased rate of glucose uptake [18]. Glycolytic and oxidative mitochondrial metabolic enzyme gene expression variations in live cells are little studied. Cirrhosis patients' poor prognoses may be linked to the occurrence of an aerobic glycolytic metabolism in the pre-cancerous stages of hepatic carcinogenesis, according to new research. This is why we evaluated the expression levels of enzymes required for glycolytic and mitochondrial metabolism in liver samples from cirrhotic and HCC patients available in six open source data sets.

Patients with malignant cancer die from liver cancer at the fourth-highest rate [25,26]. About 90% of all liver cancers are hepatocellular carcinomas (HCCs), which are often discovered too late and have a dismal prognosis. As a result, early detection of HCC is critical to a patient's prognosis and survival [27]. Currently, the diagnosis of HCC is made by laboratory and imaging modalities [6,28]. Current blood biomarkers and modalities such as AFP and imaging have shown low diagnosis accuracy for early stages of HCC [29]. A liver biopsy can only be used as a diagnostic tool in clinical practice if imaging methods fail to reliably diagnose HCC [30]. The success rate of a diagnosis may be decreased if the biopsy site is erroneous [31]. Pathologists must therefore devise a novel technique or diagnostic characteristic to enable them detect early HCC in biopsy specimens, even if the samples have been poorly obtained. When cirrhosis or normal tissue is present in HCC patients, the malignant tissues are likely to have an impact, leading to molecular characteristics that resemble those of cancerous tissues [32,33].

Liver cancer contributes significantly to the global cancer burden. Many countries have seen an increase in the disease's prevalence during the last few decades. As the most common kind of liver cancer, hepatocellular carcinoma (HCC) is responsible for the vast majority of cases and fatalities. These two hepatitis B and hepatitis C viruses remain the most important global risk factors for HCC, but their impact is expected to reduce in the near future. The impact of HBV immunization of infants, which has already been observed in several countries' young people, will become more noticeable as the vaccinated cohorts age. Effective treatments for persistent HBV and HCV infections should also lower the incidence of HCC linked with viral infection. Diabetes type II and non-alcoholic fatty liver disease (NAFLD) are both on the rise in prevalence, and this could become a key contributor in the rise in the global incidence of hepatocellular carcinoma. Aflatoxin poisoning of food crops in various regions of the world, as well as excessive alcohol intake, remain stubborn risk factors. Primary prevention

measures to reduce the prevalence of obesity, diabetes, and mycotoxin growth are equally as critical as attempts to improve early detection and treatment of HCC [34]

A large number of existing diagnostic signatures are based primarily on risk ratings derived from signature gene expression [35,36,37,38,39], which are particularly susceptible to measurement batch effects [40]. Thanks to Eddy *et al* (45), which originally presented the REO-based technique [41,42,43,44], REO-based strategy is extremely robust against experimental batch effects [46,47,48] and platform differences [49], although RNA that certain inherent correlations between these genes are not revealed. Even more importantly, the accuracy of HCC diagnosis needs to be enhanced further yet [58].

If you're looking to identify hidden patterns, a machine learning method is a fantastic option. These samples were contaminated by deterioration [50], and there was no way to be sure where they came from [51,52,53,54]. This has led to the early detection of HCC, gastric cancer [56], and colorectal cancer using REOs [57]. In 2018, Ao *et al.* [55] used the within-sample REOs to identify 19 gene pairings. These genes could improve early detection of HCC utilizing biopsy specimens, even if the specimens are improperly sampled. Because it is so simple to develop, many bioinformatics specialists employ the rule to diagnose HCC using REOs [59,60,61,62,63,64]. HCC in REOs can now be detected using a machine learning-based technique. – mRMR was used to eliminate redundant REOs and establish a diagnostic signature comprising 11 gene pairs (minimal redundancy maximum relevance). Additionally, these gene pairs were tested in different datasets to see if they might diagnose HCC. According to Ao *et al* and coworkers, mRMR-based. 11-pair signature is superior to the existing 19-pair signature, which was also developed by them [55].

Body of the article

As of now, the race is on to publish studies that reveal more effective diagnostic factors than AFP in detecting HCC. The enzyme alpha-L fucosidase was one of these variables (AFU). At the experimental and human levels, we compared AFU to AFP for percent specificity and percent diagnostic accuracy percent. There were 90, 92, and 91 AFU values at the cutoff value of 5, however there were only 60, 76.8, and 68.8 AFP values at the cutoff value of 60 [5]. It is only in main HCC that AFP is elevated, but in secondary HCC, AFP is absent, indicating a more effective panel of seromarkers in different stages of HCC[4]. AFP is only elevated in first HCC, but in secondary HCC, AFP is absent, indicating that AFP is more effective in different stages. It was found that biochemical staging of HCC was more convenient than histological staging in certain of our studies. To sum it up: AFP increases as the number of human HCC lesions increases while the serum total glycosaminoglycans, free glucose amine, and total sialic acid all progress [65]. In addition, serum serotonin levels were found to be more predictive of experimental HCC progression than AFP [66]. HCC staging could be improved by using somatostatin receptor RNA and protein instead of somatostatin because of the short half-life of the hormone [67]. There is a strong link between cancer cell metastatic potential and lysosomal membrane integrity, as well as treatment responsiveness and resistance [68].

Conclusion

It appears that AFP blood levels used for surveillance, early detection, diagnosis, and follow-up after therapy are unreliable, which is why care of liver cancer, whether primary or secondary HC, is never encouraging. Every time a malignancy has progressed, different radiological procedures are used. Biochemical changes in hepatocytes may provide an adequate tool for prevention and/or predication among those at high risk for developing HCV. A biochemical panel should be used instead of AFP in patients at high risk for HC, such as viral hepatitis or liver fibrosis. When metastasis to the liver is predicted from non-hepatic sites like the colon, breasts, or lungs following surgical removal, it is difficult to predict if the cancer

will return or if it will spread elsewhere in the body. In addition to AFP testing, we believe that the patient should be exposed to a panel of indicators including AFU, total glycosaminoglycans, total sialic acid, free glucosamine, gamma carboxylate, 5′-nucleotidase, and leucine aminopeptidase activities, as well as serotonin levels. However, although the addition of tissue somatostatin protein concentration would be quite beneficial in our screening job, we are trying to avoid using biopsies. The therapy of liver cancer is more likely to be successful when a high-risk patient or one who is currently undergoing treatment is brought before this panel.

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